

SEQUENCE LISTING

<110> KaloBios, Inc.

<120> TRANSACTIVATION SYSTEM FOR MAMMALIAN CELLS

<130> CELA001/01WO

<160> 23

<170> PatentIn version 3.2

<210> 1

<211> 236

<212> PRT

<213> hamster

<400> 1

Met Ala Gln Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
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Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Val
 20 25 30

Gly Asp Val Asp Ala Ala Pro Leu Gly Ala Ala Pro Thr Pro Gly Ile
 35 40 45

Phe Ser Phe Gln Pro Glu Ser Asn Pro Thr Pro Ala Val His Arg Asp
 50 55 60

Met Ala Ala Arg Thr Ser Pro Leu Arg Pro Ile Val Ala Thr Thr Gly
 65 70 75 80

Pro Thr Leu Ser Pro Val Pro Pro Val Val His Leu Thr Leu Arg Arg
 85 90 95

Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe Ala Glu Met
 100 105 110

Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly Arg Phe Ala
 115 120 125

Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile
 130 135 140

Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu Ser Val Asn
 145 150 155 160

Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp Met Thr Glu
 165 170 175

Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn Gly Gly Trp
 180 185 190

Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Val Arg Pro Leu Phe Asp
 195 200 205

Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala Leu Val Gly
 210 215 220

Ala Cys Ile Thr Leu Gly Thr Tyr Leu Gly His Lys
 225 230 235

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Met Ala Gln Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
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Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Val
 20 25 30

Gly Asp Val Asp Ala Ala Ala Ala Ala Ala Ser Pro Val Pro Pro Val
 35 40 45

Val His Leu Thr Leu Arg Arg Ala Gly Asp Asp Phe Ser Arg Arg Tyr
 50 55 60

Arg Arg Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe
 65 70 75 80

Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp
 85 90 95

Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val
 100 105 110

Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn
 115 120 125

Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp
 130 135 140

Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro
 145 150 155 160

Ser Val Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu
 165 170 175

Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Thr Tyr Leu
 180 185 190

Gly His Lys
 195

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 <212> DNA
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<210> 4
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 <212> PRT
 <213> Human adenovirus type 5

<400> 4

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 1 5 10 15

Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu Ala Asp Asn Leu
 20 25 30

Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu His Asp
 35 40 45

Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln
 50 55 60

Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gly Ile Asp Leu
 65 70 75 80

Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser
 85 90 95

Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met
 100 105 110

Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Gly His Glu Ala Gly
 115 120 125

Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Glu Glu Phe Val Leu
 130 135 140

Asp Tyr Val Glu His Pro Gly His Gly Cys Arg Ser Cys His Tyr His
 145 150 155 160

Arg Arg Asn Thr Gly Asp Pro Asp Ile Met Cys Ser Leu Cys Tyr Met
 165 170 175

Arg Thr Cys Gly Met Phe Val Tyr Ser Pro Val Ser Glu Pro Glu Pro
 180 185 190

Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg Pro Lys
 195 200 205

Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser Arg Glu
 210 215 220

Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn Thr Pro
 225 230 235 240

Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro Val Ala
 245 250 255

Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu Asp Leu
 260 265 270

Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg Pro Arg
 275 280 285

Pro

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 <212> DNA
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<213> Artificial

<220>
<223> primer

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<212> DNA
<213> Artificial

<220>
<223> primer

<400> 7
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<212> DNA
<213> Artificial

<220>
<223> primer

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<210> 9
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<212> DNA
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<220>
<223> primer

<400> 9
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<223> primer

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 <220>
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 <220>
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 <213> Human adenovirus type 5

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 <212> DNA
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<220>
 <223> primer

<400> 16
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<210> 17
 <211> 32
 <212> DNA
 <213> Artificial

<220>
 <223> primer

<400> 17
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<210> 18
 <211> 2824
 <212> DNA
 <213> Homo sapiens

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ccgc 2824

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<210> 19
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<212> PRT
<213> Homo sapiens

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<400> 19

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Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala
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Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu Glu Asp
20          25          30

```

```

Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
35          40          45

```

```

Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
50          55          60

```

```

Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
65          70          75          80

```

```

Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
85          90          95

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Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Arg Val Asp Leu Asp Glu
 100 105 110

Met Ser Phe Thr Leu Leu Ser Tyr Arg Lys Thr Tyr Glu Ile Ser Val
 115 120 125

His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
 130 135 140

Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
 145 150 155 160

Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
 165 170 175

Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
 180 185 190

Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
 195 200 205

Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp
 210 215 220

Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys
 225 230 235 240

Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly
 245 250 255

Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg
 260 265 270

Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val
 275 280 285

Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly
 290 295 300

Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg
 305 310 315 320

Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Arg Arg Leu Phe
 325 330 335

Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu
 340 345 350

Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Ile
 355 360 365

Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln
 370 375 380

Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu
 385 390 395 400

Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu
 405 410 415

Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys
 420 425 430

Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu
 435 440 445

Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu
 450 455 460

Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn
 465 470 475 480

Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala
 485 490 495

Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu
 500 505 510

Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe
 515 520 525

Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg
 530 535 540

Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser
 545 550 555 560

Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser
 565 570 575

Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu
 580 585 590

Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser
 595 600 605

Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser
 610 615 620

Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys
 625 630 635 640

Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg
 645 650 655

Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu
 660 665 670

His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu
 675 680 685

Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met
 690 695 700

Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys
 705 710 715 720

Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln
 725 730 735

Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile
 740 745 750

Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile
 755 760 765

Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His
 770 775 780

Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro
785 790 795 800

Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser
805 810 815

Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu
820 825 830

Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile
835 840 845

Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu
850 855 860

Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu
865 870 875 880

Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys
885 890 895

Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln
900 905 910

Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
915 920 925

<210> 20
<211> 1010
<212> DNA
<213> Homo sapiens

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tgttttagaaa acagagtggc agtgcttgaa aatcaaaaca agacattgat tgaggagcta      960
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<210> 21
<211> 326
<212> PRT
<213> Homo sapiens

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<400> 21

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Met Thr Met Asp Ser Gly Ala Asp Asn Gln Gln Ser Gly Asp Ala Ala
1              5              10              15

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Val Thr Glu Ala Glu Asn Gln Gln Met Thr Val Gln Ala Gln Pro Gln
          20              25              30

```

```

Ile Ala Thr Leu Ala Gln Val Ser Met Pro Ala Ala His Ala Thr Ser
          35              40              45

```

```

Ser Ala Pro Thr Val Thr Leu Val Gln Leu Pro Asn Gly Gln Thr Val
          50              55              60

```

```

Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser Val Ile Gln Ser
65              70              75              80

```

```

Pro Gln Val Gln Thr Val Gln Ile Ser Thr Ile Ala Glu Ser Glu Asp
          85              90              95

```

```

Ser Gln Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Ile
          100              105              110

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```

Leu Ser Arg Arg Pro Ser Phe Arg Lys Ile Leu Asn Asp Leu Ser Ser
          115              120              125

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Asp Ala Pro Gly Val Pro Arg Ile Glu Glu Glu Lys Ser Glu Glu Glu
 130 135 140

Ala Ser Ala Pro Ala Ile Thr Ala Val Ala Val Pro Thr Pro Ile Tyr
 145 150 155 160

Arg Thr Ser Ser Gly Gln Tyr Ile Thr Ile Thr Gln Arg Gly Ala Ile
 165 170 175

Gln Leu Ala Ser Asn Gly Thr Asp Gly Val Gln Gly Leu Gln Thr Leu
 180 185 190

Thr Met Ala Asn Ala Ala Ala Thr Gln Pro Gly Thr Thr Ile Leu Gln
 195 200 205

Tyr Ala Gln Thr Thr Asp Gly Gln Gln Ile Leu Val Pro Ser Asn Gln
 210 215 220

Val Val Val Gln Ala Ala Ser Gly Asp Val Gln Thr Tyr Gln Ile Arg
 225 230 235 240

Thr Ala Pro Thr Ser Thr Ile Ala Pro Gly Val Val Met Ala Ser Ser
 245 250 255

Pro Ala Leu Pro Thr Gln Pro Ala Glu Glu Ala Ala Arg Lys Arg Glu
 260 265 270

Val Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu Cys Arg Arg Lys
 275 280 285

Lys Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val Ala Val Leu Glu
 290 295 300

Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala Leu Lys Asp Leu
 305 310 315 320

Tyr Cys His Lys Ser Asp
 325

<210> 22
 <211> 43
 <212> DNA
 <213> Artificial

<220>

<223> primer

<400> 22

cccgaattcg ccgccacccat gaccatggac tctggagcag aca

43

<210> 23

<211> 30

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 23

gtcgacccaa attaatctga tttgtggcag

30

Primer 14: GTCAAGCAAGCTTGCCGCCACCATGAGACATATTATCTGCCACGG
(SEQ ID NO: 24)

Primer 15: CGCAGTCTCGAGTTATGGCCTGGGGCGTTTACAGCTC (SEQ ID NO:
25)

Primer 16: CACCTACCCTTCACGAACTGCATGATTTAGACGTGACGGCC (SEQ ID
NO: 26)

Primer 17: GGCCGTCACGTCTAAATCATGCAGTTCGTGAAGGGTAGGTG (SEQ ID
NO: 27)

Primer 18: CGGAGGTGATCGATCTTACCGGCCACGAGGCTGGCTTTCCAC (SEQ
ID NO: 28)

Primer 19: GTGGAAAGCCAGCCTCGTGGCCGGTAAGATCGATCACCTCCG (SEQ
ID NO: 29)

Primer 20: GTCAAGCAAGCTTGCCGCCACCATGACCATGGAATCTGGAGC (SEQ
ID NO: 30)

Primer 21: CGCAGTGGATCCTTAATCTGATTTGTGGCAGTAAAGG (SEQ ID NO:
31)

Primer 22: GTCATTCAAAATTTTCCTGAAGGAAGGCCTCCTTGAAAG (SEQ ID NO: 32)

Primer 23: TCTTTCAAGGAGGCCTTCCTTCAGGAAAATTTTGAATGAC (SEQ ID NO: 33)

Primer 24: GGCATTCCAAGCTTACTGTTGGTAAAGCCGCCACCATGGAGGCTTGGG AGTGTTTGG (SEQ ID NO: 34)

Primer 25: GATCGACTCTAGATCATTCCTCCGAGGGTCCAGGCCGG (SEQ ID NO: 35)

Primer 26: TAAAGCCACCATGGCTCAAGCTGGGAGAACAGGGTATG (SEQ ID NO: 36)

Primer 27: GATCGACTCTAGATCACTTGTGGCCCAGGTAGGTACCC (SEQ ID NO: 37)

Primer 28: GTGGGAGATGTGGACGCCGCGGCCGCGGCCGCGAGCCCCGTGCCAC CTGTGGTCC (SEQ ID NO: 38)

Primer 29: GGACCACAGGTGGCACGGGGCTCGCGGCCGCGGCCGCGGCGTCCAC ATCTCCAC (SEQ ID NO: 39)

(From Figure 10) Nucleotide coding sequence of Ela cDNA (SEQ ID NO: 40):

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1  aagcttgccg ccacatgag acatattatc tgccacggag gtgttattac
   HindIII      M R H I I C H G G V I
51  cgaagaaatg gccgccagtc tttggacca gctgatcgaa gaggtactgg
   T E E M A A S L L D Q L I E E V L
101 ctgataatct tccacctcct agccattttg aaccacctac ccttcacgaa
   A D N L P P P S H F E P P T L H E
151 ctgtatgatt tagacgtgac ggcccccgaa gatcccaacg aggaggcgg
   L Y D L D V T A P E D P N E E A
201 ttgcagatt tttccgact ctgtaatgtt ggcggtgcag gaagggattg
   V S Q I F P D S V M L A V Q E G I
251 acttactcac tttccgccg gcgcccgggt ctccggagcc gcctcacctt
   D L L T F P P A P G S P E P P H L

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301 tcccggcagc ccgagcagcc ggagcagaga gccttgggtc cggtttctat
 S R Q P E Q P E Q R A L G P V S
 351 gccaaacctt gtaccggagg tgatcgatct tacctgccac gaggtggct
 M P N L V P E V I D L T C H E A G
 401 ttccaccag tgacgacgag gatgaagagg gtgaggagt tgtgttagat
 F P P S D D E D E E G E E F V L D
 451 tatgtggagc acccgggca cggttgcagg tctgtcatt atcaccggag
 Y V E H P G H G C R S C H Y H R
 501 gaatacgggg gacccagata ttatgtgttc gctttgctat atgaggacct
 R N T G D P D I M C S L C Y M R I
 551 gtggcatgtt tgtctacagt cctgtgtctg aacctgagcc tgagcccag
 C G M F V Y S P V S E P E P E P E
 601 ccagaaccgg agcctgcaag acctaccgc cgtcctaaaa tggcgctgc
 P E P E P A R P T R R P K M A P
 651 tatectgaga cgcccgacat cacctgtgtc tagagaatgc aatagtagta
 A I L R R P T S P V S R E C N S S
 701 cggatagctg tgactccggt ccttctaaca cacctcctga gataccccg
 T D S C D S G P S N T P P E I H P
 751 gtgtcccg cgtgtcccat taaaccagt gccgtgagag ttggtggcg
 V V P L C P I K P V A V R V G G
 801 tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac
 R R Q A V E C I E D L L N E P G Q
 851 ctttggactt gagctgtaaa cgccccaggc cataactcga g
 P L D L S C K R P R P - *XhoI*

(From Figure 11) Nucleotide coding sequence of E1A mutant
 Y47H (SEQ ID NO: 41):

1 aagcttgccg ccaccatgag acatattatc tgccacggag gtgttattac
HindIII M R H I I C H G G V I
 51 cgaagaaatg gccgccagtc ttttgacca gctgatcgaa gaggtactgg
 T E E M A A S L L D Q L I E E V L
 101 ctgataatct tccacctct agccattttg aaccacctac ccttcacgaa
 A D N L P P P S H F E P P T L H E
 151 ctgcatgatt tagacgtgac ggcccccgaa gatcccaacg aggaggcgg
 L H D L D V T A P E D P N E E A
 201 ttgcgagatt tttcccgact ctgtaatgtt ggcgggtgcag gaagggattg
 V S Q I F P D S V M L A V Q E G I
 251 acttactcac ttttccggcg gcgccccggt ctccggagcc gcctcacctt
 D L L T F P P A P G S P E P P H L
 301 tcccggcagc ccgagcagcc ggagcagaga gccttgggtc cggtttctat
 S R Q P E Q P E Q R A L G P V S
 351 gccaaacctt gtaccggagg tgatcgatct tacctgccac gaggtggct

M P N L V P E V I D L T C H E A G
 401 ttccacccag tgacgacgag gatgaagagg gtgaggagtt tgtgttagat
 F P P S D D E D E E G E E F V L D
 451 tatgtggagc accccgggca cgttgcagg tctgtcatt atcaccggag
 Y V E H P G H G C R S C H Y H R
 501 gaatacgggg gacccagata ttatgtgttc gctttgctat atgaggacct
 R N T G D P D I M C S L C Y M R T
 551 gtggcatgtt tgtctacagt cctgtgtctg aacctgagcc tgagcccag
 C G M F V Y S P V S E P E P E P E
 601 ccagaaccgg agcctgcaag acctaccgcg cgtcctaaaa tggcgctgc
 P E P E P A R P T R R P K M A P
 651 taccctgaga cgcccgacat cacctgtgtc tagagaatgc aatagtagta
 A I L R R P T S P V S R E C N S S
 701 cggatagctg tgactccggt ccttctaaca cacctcctga gataccccg
 T D S C D S G P S N T P P E I H P
 751 gtgggtccgc tgtgccccat taaaccagtt gccgtgagag ttggtgggcg
 V V P L C P I K P V A V R V G G
 801 tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac
 R R Q A V E C I E D L L N E P G Q
 851 ctttggactt gagctgtaaa cgccccaggc cataactcga g
 P L D L S C K R P R P - *XhoI*

(From Figure 12) Nucleotide coding sequence of hamster CREB-
 B cDNA (SEQ ID NO: 42):

1 aagcttgccg ccaccatgac catggaatct ggagcagaca accagcagag
HindIII M T M E S G A D N Q Q
 51 tggagatgct gctgtaacag aagctgaaaa tcaacaaatg acagctcaag
 S G D A A V T E A E N Q Q M T A Q
 101 cccaaccaca gattgccaca ttagcccagg tatccatgcc agcagctcat
 A Q P Q I A T L A Q V S M P A A H
 151 gcgacatcat ctgtctccac tgtaacctta gtgcagctgc ccaatgggca
 A T S S A P T V T L V Q L P N G
 201 gacagtccaa gtccatggag ttattcaggc ggcccagcca tcagttattc
 Q T V Q V H G V I Q A A Q P S V I
 251 agtctccaca agtccaaca gttcagtctt cctgtaagga cttaaaaaga
 Q S P Q V Q T V Q S S C K D L K R
 301 cttttctccg gaactcagat ttcaactatt gcagaaagtg aggattcaca
 L F S G T Q I S T I A E S E D S
 351 ggaatctgtg gatagtgtaa ctgattccca aaagcgaagg gaaattcttt
 Q E S V D S V T D S Q K R R E I L
 401 caaggaggcc ttctacagg aaaatttga atgacttatc ttctgatgca

S R R P S Y R K I L N D L S S D A
 451 ccaggggtgc caaggattga agaagaaaag tcggaagagg agacttcagc
 P G V P R I E E E K S E E E T S
 501 ccctgccatc accactgtga cagtgccaac tccgatttac cagacaagca
 A P A I T T V T V P T P I Y Q T S
 551 gtgggcagta tattgccatt acccagggag gagctataca gctggctaac
 S G Q Y I A I T Q G G A I Q L A N
 601 aatgggtaccg atgggggtaca gggccttcag acattaacca tgaccaatgc
 N G T D G V Q G L Q T L T M T N
 651 agctgccact cagccgggta ccactattct acagtatgca cagaccactg
 A A A T Q P G T T I L Q Y A Q T T
 701 atggacagca gattctagtgc cccagcaacc aagtgtgtgt tcaagctgcc
 D G Q Q I L V P S N Q V V V Q A A
 751 tctggcgtatg tacaacata ccaaattcgt acagcaccca ctgacccat
 S G D V Q T Y Q I R T A P T S T
 801 cgcccctgga gttgttatgg catctctccc agcatttct acgcagcctg
 I A P G V V M A S S P A L P T Q P
 851 ctgaagaagc agcccgggaag agagagggtc gtctaataaa gaacagggaa
 A E E A A R K R E V R L M K N R E
 901 gcagcaagag aatgtcgtag aaagaagaaa gaatatgtga aatgtttaga
 A A R E C R R K K K E Y V K C L
 951 gaacagagtgc gcagtgcctg aaaacaaaa caagacattg attgaggagc
 E N R V A V L E N Q N K T L I E E
 1001 taaaagcact taaggacctt tactgccaca aatcagatta aggatcc
 L K A L K D L Y C H K S D - *Bam*HI

(From Figure 13) Nucleotide coding sequence of hamster CREB-
 B mutant Y134F (SEQ ID NO: 43):

1 aagcttgccg ccaccatgac catggaatct ggagcagaca accagcagag
*Hind*III M T M E S G A D N Q Q
 51 tggagatgct gctgtaacag aagctgaaaa tcaacaaatg acagctcaag
 S G D A A V T E A E N Q Q M T A Q
 101 cccaaccaca gattgccaca ttagcccagg tatccatgcc agcagctcat
 A Q P Q I A T L A Q V S M P A A H
 151 ggcacatcat ctgctccac tgtaacctta gtgcagctgc ccaatgggca
 A T S S A P T V T L V Q L P N G
 201 gacagtccaa gtccatggag ttattcaggc ggcccagcca tcagttattc
 Q T V Q V H G V I Q A A Q P S V I
 251 agtctccaca agtccaaaca gttcagtctt cctgtaagga cttaaaaaga
 Q S P Q V Q T V Q S S C K D L K R
 301 cttttctccg gaactcagat ttcaactatt gcagaaagtg aggattcaca
 L F S G T Q I S T I A E S E D S

351 ggaatctgtg gatagtgtaa ctgattccca aaagcgaagg gaaattcttt
 Q E S V D S V T D S Q K R R E I L
 401 caaggaggcc ttctccagg aaaatttga atgacttate ttctgatgca
 S R R P S F R K I L N D L S S D A
 451 ccaggggtgc caaggattga agaagaaaag tcggaagagg agacttcagc
 P G V P R I E E E K S E E E T S
 501 ccctgccatc accactgtga cagtgccaac tccgatttac cagacaagca
 A P A I T T V T V P T P I Y Q T S
 551 gtgggcagta tattgccatt acccagggag gagctataca gctggctaac
 S G Q Y I A I T Q G G A I Q L A N
 601 aatggtagcg atgggggtaca gggccttcag acattaacca tgaccaatgc
 N G T D G V Q G L Q T L T M T N
 651 agctgccact cagccgggta ccactattct acagtatgca cagaccactg
 A A A T Q P G T T I L Q Y A Q T T
 701 atggacagca gattctagt cccagcaacc aagtgtgtg tcaagctgcc
 D G Q Q I L V P S N Q V V V Q A A
 751 tctggcgtg tacaacata ccaaatcgt acagcaccca ctgacccat
 S G D V Q T Y Q I R T A P T S T
 801 cgcccctgga gttgttatgg catcctcccc agcattcct acgcagcctg
 I A P G V V M A S S P A L P T Q P
 851 ctgaagaagc agcccgaag agagagggtc gtctaataa gaacagggaa
 A E E A A R K R E V R L M K N R E
 901 gcagcaagag aatgtcgtg aaagaagaaa gaatatgtga aatgtttaga
 A A R E C R R K K K E Y V K C L
 951 gaacagagtg gcagtgcctg aaaacaaaa caagacattg attgaggagc
 E N R V A V L E N Q N K T L I E E
 1001 taaaagcact taaggacctt tactgccaca aatcagatta aggatcc
 L K A L K D L Y C H K S D - *BamHI*

(From Figure 14) Nucleotide coding sequence of E1b-19K (SEQ ID NO: 44):

1 aagcttactg ttgtaaagc cgccaccatg gaggcttggg agtgtttgga
HindIII M E A W E C L
 51 agattttct gctgtgcgta acttgcctga acagagctct aacagtacct
 E D F S A V R N L L E Q S S N S T
 101 cttggtttg gaggtttctg tggggctcat cccaggcaaa gttagtctgc
 S W F W R F L W G S S Q A K L V C
 151 agaattaagg aggattacaa gtgggaattt gaagagcttt tgaaatcctg
 R I K E D Y K W E F E E L L K S

201 tggtagctg ttgattctt tgaatctggg tcaccaggcg cttttccaag
 C G E L F D S L N L G H Q A L F Q
 251 agaaggtcat caagacttg gattttcca caccggggcg cgctgcggct
 E K V I K T L D F S T P G R A A A
 301 gctgttgctt tttgagttt tataaaggat aaatggagcg aagaaaccca
 A V A F L S F I K D K W S E E T
 351 tctgagcggg gggtacctgc tggatttct ggccatgcat ctgtggagag
 H L S G G Y L L D F L A M H L W R
 401 cggttgtgag acacaagaat cgcctgtac tgtgtcttc cgtccgccc
 A V V R H K N R L L L L S S V R P
 451 gcgataatac cgacggagga gcagcagcag cagcaggagg aagccaggcg
 A I I P T E E Q Q Q Q Q E E A R
 501 gcggcggcag gagcagagcc catggaaccc gagagccggc ctggaccctc
 R R R Q E Q S P W N P R A G L D P
 551 gggaatgac taga
 R E - *XbaI*

(From Figure 15) Nucleotide coding sequence of hamster Bcl2 deletion mutant (SEQ ID NO: 45):

NcoI
 1 ccatggctca agctgggaga acagggtatg ataaccgaga gatcgtgatg
 M A Q A G R T G Y D N R E I V M
 51 aagtacatcc attataagct gtcacagagg ggctacgagt gggatgtggg
 K Y I H Y K L S Q R G Y E W D V
 101 agatgtggac gccgcggccg cggccgcgag ccccggtcca cctgtggtcc
 G D V D A A A A A A S P V P P V V
 151 acctgaccct ccgccgggct ggggatgact tctcccgtcg ctaccgtcgc
 H L T L R R A G D D F S R R Y R R
 201 gacttcgcgg agatgtccag tcagctgcac ctgacgccct tcaccgcgag
 D F A E M S S Q L H L T P F T A
 251 gggacgcttt gctacggttg tggaggaact cttcagggat ggggtgaact
 R G R F A T V V E E L F R D G V N
 301 gggggaggat tgtggccttc tttgagttcg gtggggtcat gtgtgtggag
 W G R I V A F F E F G G V M C V E
 351 agcgtcaaca gggagatgac acccctggtg gacaacatcg ccctgtggat

S V N R E M S P L V D N I A L W
401 gaccgagtac ctgaaccggc atctgcacac ctggatccag gataacggag
M T E Y L N R H L H T W I Q D N G
451 gctgggacgc atttgtggaa ctgtacggcc ccagtgtgag gcctctgttt
G W D A F V E L Y G P S V R P L F
501 gatttctctt ggctgtctct gaagaccctg ctcagcctgg ccctggtcgg
D F S W L S L K T L L S L A L V
551 ggcctgcac actctgggta cctacctggg ccacaagtga tctaga
G A C I T L G T Y L G H K - *XbaI*

Primer 30: CGCAGTACTAGTTTATGGCCTGGGGCGTTTACAGCTC (SEQ ID
NO:46)

Primer 31: GAGCTATTCCAGAAGTAGTG (SEQ ID NO:47)